SOC-GA 2332 Intro to Stats Lab 3

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Logistics & Announcement

- **Problem Set 1** is due on Tue Sep. 29th, 11:59 pm.
- Make sure to comment on your code. You will get credit for demonstrating your thought process even if you don't get the final answer correct.

```r
knitr::opts_chunk$set(echo = TRUE)
library(tidyverse)

# Import data
weight_df <- read.csv("data/weight.csv")
```

Part 1 Review: Population and Sample

1. Write down the formula you use to calculate the following sample statistics (assume your sample size $= n$):

- Sample mean:
- Sample variance:
- Sample standard deviation:
- Standard error of sample mean:
- 95% confidence interval of the population mean:

2. You have collected a sample of 25 on BMI (Body Mass Index). The sample mean is 23 and sample variance is 4.

- What is the point estimate of the population mean?
- What is the 95% confidence interval of the population mean (round to 2 d.p.)?
- What is the 95% confidence interval of the population mean if the sample size is 10,000 (round to 2 d.p.)?

Part 2: Hypothesis and Significance Test

First, let's review the standard steps for conducting a significance test:

2.1 The standard procedure of a significance test

- 1. Formulate our research question in the null and alternative hypotheses
- 2. Select a significance level (α) (in social science, usually $\alpha = 0.05$)
- 3. Select which test statistics to use (for small samples, we use the ***t* test statistics**)

- 4. If you are collecting first-hand data, select a sample size that provides you with sufficient statistical power
- 5. Derive the **sampling distribution of the test statistic** under the assumption that **the null hypothesis is true**
- For the t test statistics, its sampling distribution is approximately the Student t distribution with $n-1$ degrees of freedom
- When n gets larger (usually $n > 30$), the t distribution is approximately a standard normal distribution (see graph below)
- The t test statistic formula is: $t = \frac{\bar{y}-\mu_0}{se}$ (μ_0 is the population mean in the null hypothesis)

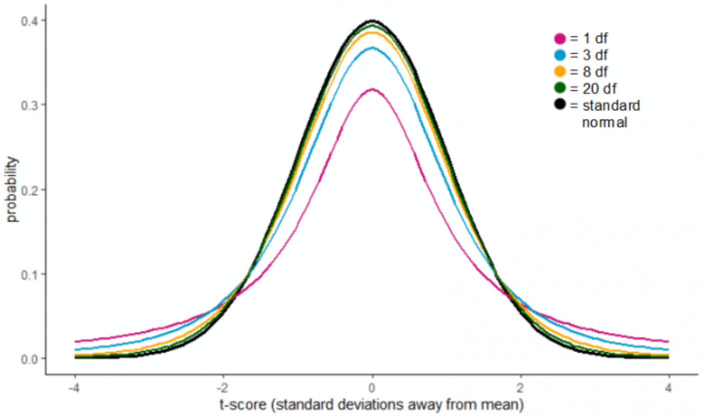


Figure 1: t distribution 1

- 6(A) Derive the critical value of t and your rejection region according to the null hypothesis
- The critical value of t (CV_t) is the value beyond which we will regard our observed t as “unusual”
- The rejection region will be $(-\infty, -|CV_t|) \cup (|CV_t|, \infty)$.
- For samples with a df ≥ 100, the critical value of t is **1.96** for a significance level at 0.05. The rejection region is $(-\infty, -1.96) \cup (1.96, \infty)$
- For samples with a df ≤ 100, you can use the “t Distribution Critical Values” table in your textbook to find out the critical value and rejection region:
  - For a **two-tailed test** that have a significance level at 0.05, we find values from the $t_{.025}$ column
  - For a **one-tailed test** that have a significance level at 0.05, we find values from the $t_{.050}$ column
- You can also use the `qt()` function in `R` to find out the critical value:
  - To find out critical value of t for a **two-tailed test**, use `qt(p = 0.5*your_alpha, df = your_degree_of_freedom)`
  - To find out critical value of t for a **one-tailed test**, use `qt(p = your_alpha, df = your_degree_of_freedom)`
  - *Note*: the `qt()` function is the quantile function for the Student t distribution in base `R` that gives the t value based on the percentile you input
- 6(B) Alternatively, you can calculate the p-value of your observed t statistic
- p-value is the probability that the test statistic equals to (or is more extreme than) what we observed

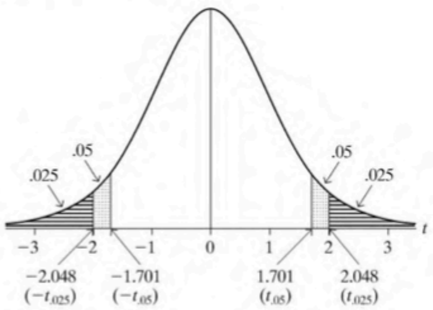


FIGURE 5.5: *t* Distribution with *df* = 28

Figure 2: t distribution 2

  - To find out the **two-tail** p-value, use `2*pt(q = observed_t, df = your_degree_of_freedom, lower.tail = FALSE)`
  - To find out the **one-tail** p-value, use `pt(q = observed_t, df = your_degree_of_freedom, lower.tail = FALSE)`

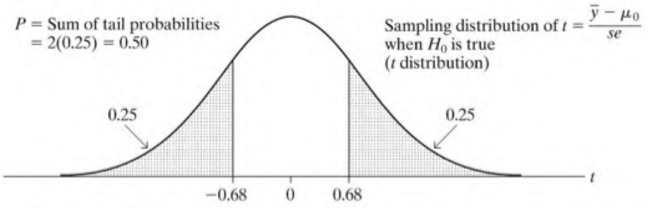


FIGURE 6.3: Calculation of *P*-Value when $t = 0.68$, for Testing H_0: $\mu = \mu_0$ against H_a: $\mu \neq \mu_0$. The *P*-value is the two-tail probability of a more extreme result than the observed one.

Figure 3: t distribution 3

- 7. Make a conclusion about whether to reject the null hypothesis
  - You can use this online tool to visualize a t-test

Exercise

With $\mu_0 = 0$, $\bar{y} = 1.54$, sample $n = 27$, $s = 3.25$, derive:
(1) The t test statistic
(2) The critical value of t given H_0 is true
(3) Your rejection region
(4) p-value
(5) Your conclusion of the significance test

```
## you can code your answer here
```

2.2 One-sample t-test using R

- When do you use one-sample t-test?
- R provides a simple function `t.test()` to perform hypothesis testing using the t test statistics

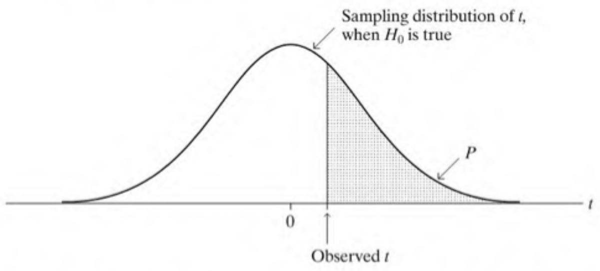


FIGURE 6.4: Calculation of P-value in Testing H_0: $\mu = \mu_0$ against H_a: $\mu > \mu_0$. The P-value is the probability of values to the right of the observed test statistic.

Figure 4: t distribution 4

- For example, the data object `weight_df` we just imported records the weight change of anorexic patients who went through therapy programs, and we want to know whether these therapies are effective.

```
## check data
head(weight_df)
```

```
##   subj therapy before after change
## 1    1       b   80.5  82.2    1.7
## 2    2       b   84.9  85.6    0.7
## 3    3       b   81.5  81.4   -0.1
## 4    4       b   82.6  81.9   -0.7
## 5    5       b   79.9  76.4   -3.5
## 6    6       b   88.7 103.6   14.9
```

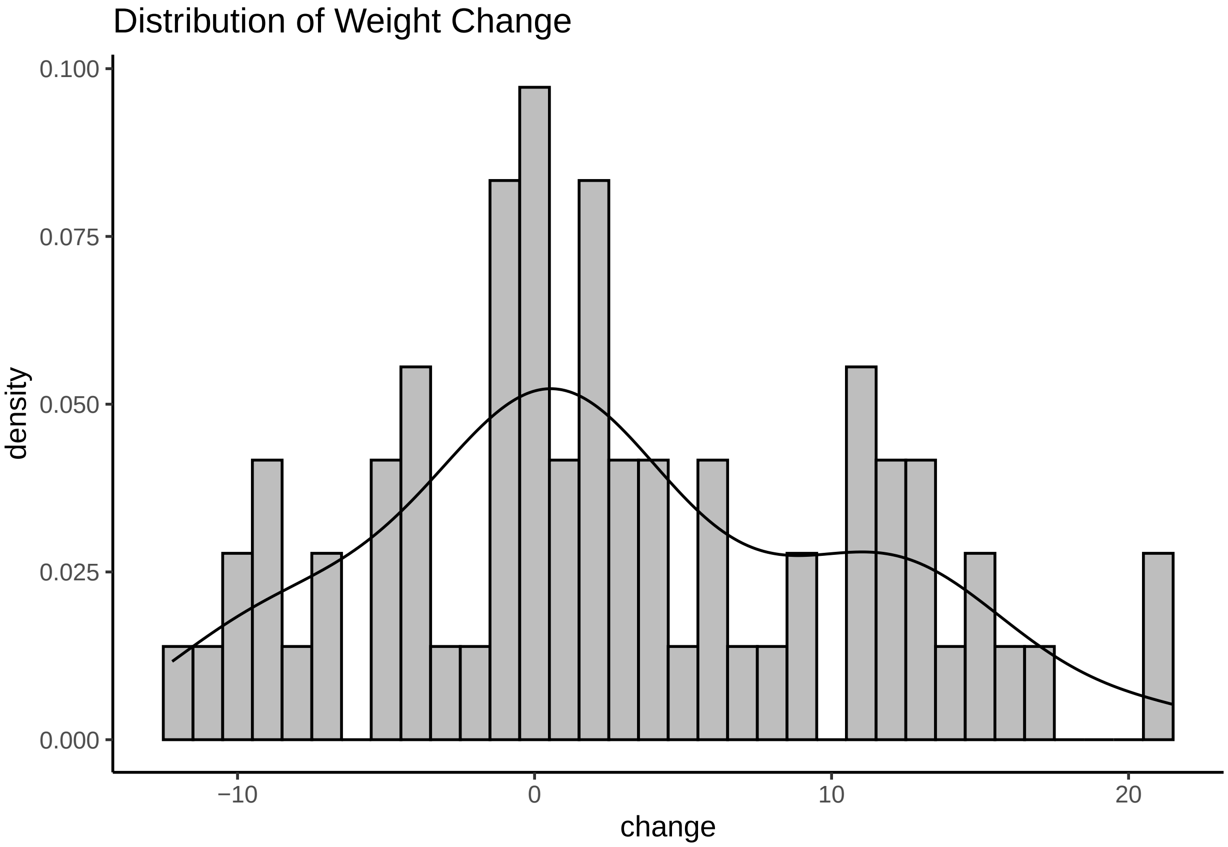
- Before performing any statistical test, it will be useful to (1) check the descriptive statistics and (2) plot the variables of interest.

```
## check descriptive statistics of all variables
summary(weight_df)
```

```
##       subj         therapy              before          after       
##  Min.   : 1.00   Length:72          Min.   :70.00   Min.   : 71.30  
##  1st Qu.:18.75   Class :character   1st Qu.:79.60   1st Qu.: 79.33  
##  Median :36.50   Mode  :character   Median :82.30   Median : 84.05  
##  Mean   :36.50                      Mean   :82.41   Mean   : 85.17  
##  3rd Qu.:54.25                      3rd Qu.:86.00   3rd Qu.: 91.55  
##  Max.   :72.00                      Max.   :94.90   Max.   :103.60  
##      change       
##  Min.   :-12.200  
##  1st Qu.: -2.225  
##  Median :  1.650  
##  Mean   :  2.764  
##  3rd Qu.:  9.100  
##  Max.   : 21.500  
```

```
## plot histogram and density curve
weight_df %>%
  ggplot(aes(x = change, y=..density..)) +
  geom_histogram(binwidth = 1, fill = "grey", color = "black") +
  geom_density() +
  labs(title = "Distribution of Weight Change") +
  theme_classic()
```

```
## Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(density)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



- We test:

$$H_0 : \mu_{\text{change}} = 0$$

- the mean weight change is 0 against:

$$H_{\text{a1}} : \mu_{\text{change}} \neq 0$$

- the mean weight change is not 0, a two-tailed test:

$$H_{\text{a2}} : \mu_{\text{change}} > 0$$

- the mean weight change is larger than 0, a one-tailed test, using the following code:

```
## mean of weight change
mean(weight_df$change)
```

```
## [1] 2.763889
```

```
# ---- one sample two-tail t-test ---- #
two_tail_t <- t.test(
  weight_df$change,           # the sample value vector that you want to test
  mu = 0,                     # mean given by your null hypothesis
  alternative = "two.sided",  # direction of alternative hypothesis
  conf.level = 0.95           # significance level
  )

## extract test statistic
two_tail_t$statistic
```

```
##        t
## 2.93757
```

```
## extract p-value
two_tail_t$p.value
```

```
## [1] 0.004457718
```

```
## extract the confidence interval of the mean
two_tail_t$conf.int
```

```
## [1] 0.8878354 4.6399424
## attr(,"conf.level")
## [1] 0.95
```

```
## display full result
two_tail_t
```

```
##
##  One Sample t-test
##
## data:  weight_df$change
## t = 2.9376, df = 71, p-value = 0.004458
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.8878354 4.6399424
## sample estimates:
## mean of x
##  2.763889
```

```
# ---- one sample one-tail t-test ---- #
t.test(weight_df$change,
       mu = 0,
       alternative = "greater",
       conf.level = 0.95)
```

```
##
##  One Sample t-test
##
## data:  weight_df$change
## t = 2.9376, df = 71, p-value = 0.002229
## alternative hypothesis: true mean is greater than 0
## 95 percent confidence interval:
##  1.195825      Inf
## sample estimates:
## mean of x
##  2.763889
```

Exercise

The institution that offers therapy programs to the anorexic patients claims that their treatment will lead to a weight increase of 4 lbs. Use the `weight_df` data and with $\alpha = 0.05$, perform both a two-tailed and a one-tailed test:

$$H_0 : \mu_{\text{change}} = 4$$

against

$$H_{\text{a1}} : \mu_{\text{change}} \neq 4 \text{ and } H_{\text{a2}} : \mu_{\text{change}} < 4$$

- Report your hypothesis testing result.
- *Hint:* Make sure you put correct arguments for your `t.test()` function! (Are you testing for "two.sided", "less", or "greater"? What's your `mu`?)

```
## you can code your answer here
```

Part 3: Comparing the Mean of Two Groups (Two-sample t-test)

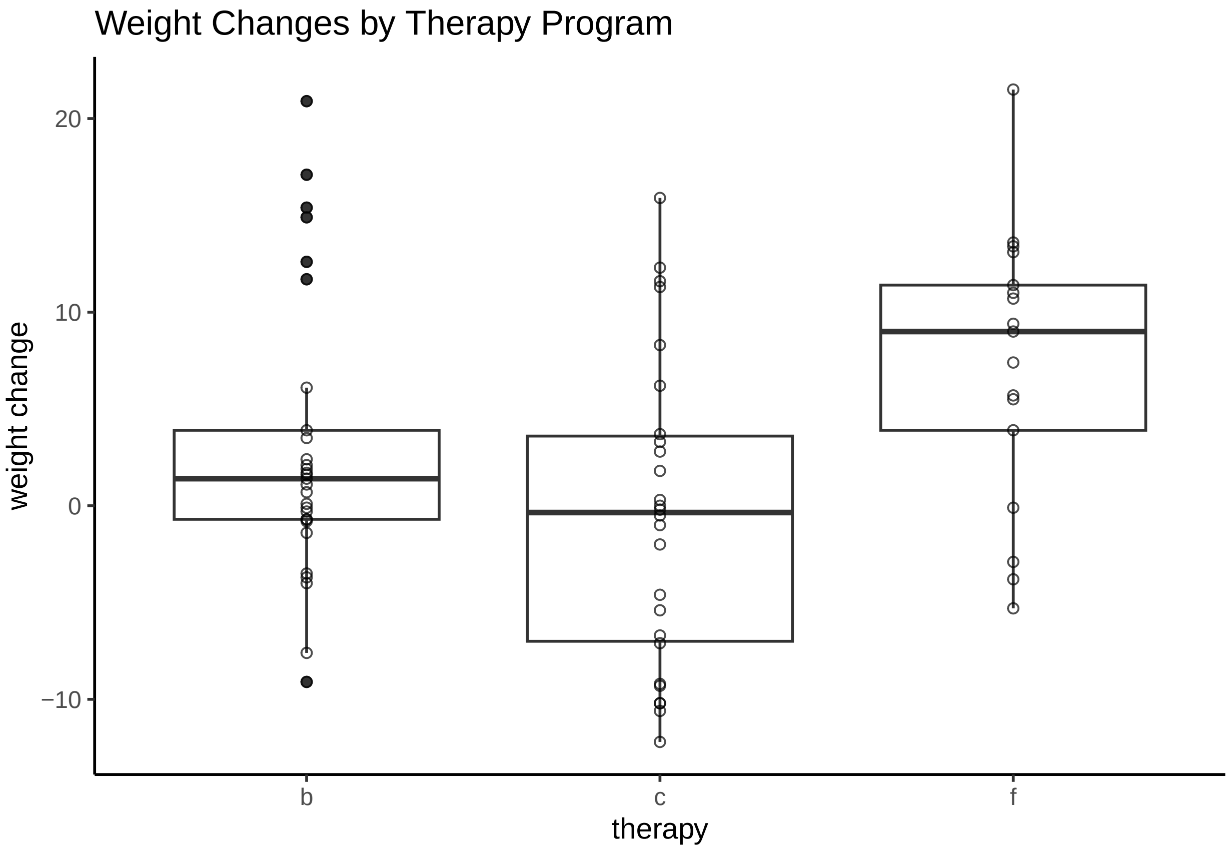
3.1 Two independent samples

In the case of comparing the mean of two independent samples, we follow the same procedures as the one sample t-test, except the statistics for finding the t test statistics change. We will not review all the formulas here. Please review lecture slides and the textbook.

Using `R`, we can perform a two-sample t-test by using the same `t.test()` function but adding a second sample mean vector.

For example, in treating anorexic patients, three different therapies are used. We can plot a boxplot to visualize how weight changes differ across these therapies.

```
## box plot
weight_df %>%
  ggplot(aes(x = therapy, y = change)) +
  geom_boxplot() +
  geom_point(shape = 1, alpha = 0.7) +
  labs(title = "Weight Changes by Therapy Program",
       y = "weight change") +
  theme_classic()
```



It looks like therapy f tends to result in a higher weight increase compared to other therapies. Let's use a two-sample t-test to see if the mean weight change in therapy f is statistically different from that in therapy c:

$$H_0 : \mu_f - \mu_c = 0$$

against

$$H_a : \mu_f - \mu_c \neq 0$$

```
## filter data for each therapy
weight_f <- weight_df %>% filter(therapy == "f")
weight_c <- weight_df %>% filter(therapy == "c")

# ---- two-group independent two-tailed t-test ---- #
t.test(
  x = weight_f$change,           # mean value vector from the first sample
  y = weight_c$change,           # mean value vector from the second sample
  mu = 0,
  # mean difference given by your null hypothesis
  alternative = "two.sided"      # direction of alternative hypothesis
)
```

```
##
##  Welch Two Sample t-test
##
## data:  weight_f$change and weight_c$change
## t = 3.2992, df = 36.979, p-value = 0.002152
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   2.976597 12.452815
## sample estimates:
## mean of x mean of y
##  7.264706 -0.450000
```

Note: The degrees of freedom of the t-distribution will be $n_0 + n_1 - 2$ **if the population variance of the two groups is equal**. This is often not a very realistic scenario. Out of this reason the Welch's approximation (which we will not define here, but can be found here if you are curious) is often used for the degrees of freedom of the t distribution. This is, in fact, the default option in the `t.test()` function that we use in `R`.

3.2 Two dependent samples

In fact, our example in the one-sample t-test in Part 2 is a two dependent sample t-test. For two dependent sample t-test, you can always create a new variable equal to the difference between the two dependent samples, like what we did in Part 2; or you can use the `t.test()` function and set the argument `paired = TRUE`.

For example, in the `weight_df` data, if we want to test whether the mean weight before the treatment is different from the mean weight after the treatment:

$$H_0 : \mu_{\text{before}} - \mu_{\text{after}} = 0$$

against

$$H_a : \mu_{\text{before}} - \mu_{\text{after}} \neq 0$$

```r
# ---- two-group dependent two-tailed t-test ---- #
t.test(
  x = weight_df$before,       # mean value vector from the first sample
  y = weight_df$after,        # mean value vector from the second sample
  mu = 0,                     # mean difference given by your null hypothesis
  paired = TRUE,              # dependent samples
  alternative = "two.sided",  # direction of alternative hypothesis
  conf.level = 0.95           # significance level
  )
```

```
##
##  Paired t-test
##
## data:  weight_df$before and weight_df$after
## t = -2.9376, df = 71, p-value = 0.004458
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -4.6399424 -0.8878354
## sample estimates:
## mean difference
##       -2.763889
```

Part 3 Exercise

Perform a two-sample two-tailed t-test for the difference between therapy b and c:

$$H_0 : \mu_b - \mu_c = 0$$

against

$$H_a : \mu_b - \mu_c \neq 0$$

```
## you can code your answer here
```